REMARKS

Claims 24-26, 28, 29, 32, 34, 37-41, 43, 44, 47, 53, 54, 59, 63, 64 and 73-105 are pending in this application. New claim 106 is added herein. Claim 106 recites a purified DNA consisting of a nucleic acid encoding an amino acid sequence of SEQ ID NO:3. Support for this claim can be found on the last full paragraph on page 28 and the carryover paragraph beginning on the bottom of page 29 of the specification. It is believed no new matter is added by this amendment.

The Office Communication of September 15, 2008 and subsequent telephone discussions with the Patent Office require Applicants to set forth the reasons why the present application should be placed in an interference with either of the two Brown et al. patents (U.S. Patent Nos. 7,071,375 and 7,314,971) and why the Applicants should be considered to be the Senior Party.

Applicant's local counsel, Peter Olexy, discussed the approach to take in responding to the office communication with ISP Larry Helms. ISP Larry Helms specifically indicated that Applicants should identify the claims of the present application that interfere, why Applicant's would be senior party if an interference were to be declared and, with respect to the '375 patent, why interference would not be proper. This was agreed upon by Applicants.

If Applicants have misunderstood any requirement that ISP Helms had in mind, Applicants will promptly provide any additional information which is required. The undersigned respectfully requests a telephone call from ISP Helms or Examiner Fox if there has been any such misunderstanding.

Accompanying this Response are five Sequence Reports providing sequence comparisons and noting sequence homology between the nucleic acid and amino acid sequences of the present application and its U.S. and foreign priority documents and the sequences of the issued patents of Brown et al. and the provisional applications to which the Brown et al. patents claim priority. The Sequence Reports are submitted as

part of a Declaration Under 37 C.F.R. 1.132 of James Coburn an expert in the preparation of such sequence comparisons. In this declaration, Mr. Coburn declares that he is the president and CEO of Harbor Consulting IP Services, Inc., a company in the business of conducting nucleic acid and amino acid sequence comparisons, and that the accompanying Sequence Reports were generated using the Basic Local Alignment Search Tool (BLAST) algorithm. Also provided is a Declaration Under 37 C.F.R. 1.132 signed by Michael Curtis, an attorney of record in this case, which states that the nucleic acid and amino acid sequences used in the sequence comparisons were taken from the cited applications and provided to Harbor Consulting IP Services, Inc. for the purpose of performing the sequence comparisons, and that the sequences provided to Harbor Consulting IP Services, Inc. are believed to be accurate copies of the sequences contained in the original applications.

Also accompanying this Response are translated copies, in English, of the foreign priority documents Japanese Application 2001-128008; Japanese Application 2001-202082; Japanese Application 2002-020083; and PCT Application PCT/JP02/04092. Certified copies of the Japanese applications were previously supplied to the Patent Office and contain the sequence listings in English. Each of the translations is accompanied by a certificate of translation in which the translator declares that the translations are a true and correct translation of the documents listed.

No Interference Should Be Declared With The 7,071,375 Patent

The claims of the present application and those of the 7,071,375 patent are generally directed to certain proteins and nucleic acid sequences encoding proteins that are reported to have function in restoration of cytoplasmic male sterility. Claims of the present application, e.g., claim 53, are specifically directed to isolated DNA sequences with such function where the nucleic acids have the sequence of SEQ ID NO:1, SEQ ID NO:2 or a nucleic acid encoding the amino acid sequence of SEQ ID NO:3. Additional claims of the present application, e.g., claim 59, are directed to an isolated DNA which encodes a protein having an amino acid sequence that is 92% or more homologous to the amino acid sequence of SEQ ID NO:3 or an isolated DNA having 95% or higher

homology to a DNA sequence encoding a protein having the amino acid sequence of SEQ ID NO:3.

Claims in the 7,071,375 patent are directed to nucleic acids having the sequence of SEQ ID NO:32, SEQ ID NO:87 (nucleotides 103,375-105,589), a nucleic acid encoding a protein having the amino acid sequence of SEQ ID NO:31 as well as a nucleic acid having at least 90% homology with the nucleic acid sequence of SEQ ID NO:32, SEQ ID NO:87 (nucleotides 103,375-105,589)(e.g., claim 1), and the nucleic acid having at least 95% homology with the nucleotide sequence shown in SEQ ID NO:32 (e.g., claim 5).

Applicants consider that there is no significant sequence homology between sequences of the present claims (SEQ ID NO:1-3) and the corresponding sequences recited in the claims of the 7,071,375 patent (SEQ ID NO: 31, 32 and 87 (nucleotides 103,375-105,589). Support for Applicants' position is found on page 1 of the attached Sequence Report for Group 1, which compares SEQ ID NO:1-3 of the present application with SEQ ID NO:31, 32 and 87 of the 7,071,375 patent. As shown in the Sequence Report for Group 1, no significant similarity was found between the sequences. As stated in the attached Declaration of James Coburn, a result of "no significant similarity was found" means that the compared sequences were so dissimilar that no meaningful alignment of the sequences could be obtained. Applicants note that the claims of the 7,071,375 patent are limited to the specifically recited nucleotide sequences, or nucleic acids having at least 90% homology with the recited sequences, and that the present claims are limited to an isolated DNA which encodes a protein having the amino acid sequence of SEQ ID NO: 3, or an isolated DNA which encodes a protein having an amino acid sequence that is 92% or more homologous to the amino acid sequence of SEQ ID NO:3.

If the Examiner considers that any of SEQ ID NO:31, 32 and 87 as recited in the claims of the 7,071,375 patent is at least 90% homologous with any of SEQ ID NO:1-3 as recited in the present claims, the Examiner is respectfully requested to identify the homology that is asserted to exist.

As a result, Applicants consider that no claim of the present application interferes with any claim of the 7,071,375 patent, because no claim of the present application is anticipated by, or obvious in view of, any claim of the 7,071,375 patent, and no claim of the 7,071,375 patent is anticipated by, or obvious in view of, any claim of the present application. If the Examiner considers that there is interfering subject matter between any of the claims of the present application, and any claim of the 7,071,375 patent, the Examiner is respectfully requested to identify the subject matter of the claim(s) of the present application that are considered to anticipate, or render obvious, claim(s) of the 7,071,375 patent, and vice versa. In the absence of such a showing of anticipation or *prima facie* obviousness by the Examiner, taking into account the specific homology limitation of the claims at issue, it is respectfully submitted that interfering subject matter does not exist between the present claims and the claims of the 7,071,375 patent.

An Interference Should Be Declared With The 7,314,971 Patent

It is believed claims 53, 105 and 106 of the present application interfere with at least claim 11 of the 7,314,971 patent.

Claim 53 of the present application recites an isolated DNA encoding the protein having the amino acid sequence of SEQ ID NO:3; an isolated DNA having the nucleotide sequence of SEQ ID NO:1; or an isolated DNA having the nucleotide sequence of SEQ ID NO:2. Claims 105 and 106 specifically recite an isolated or purified DNA consisting of a nucleic acid encoding the amino acid sequence of SEQ ID NO:3.

Claim 11 of the 7,314,971 patent recites a nucleic acid comprising a gene encoding a protein having a sequence comprising amino acids 1 to 687 of SEQ ID NO:179.

The amino acid sequence SEQ ID NO:3 of the present application is identical to SEQ ID NO:179 in the claims of the 7,314,971 patent. Both sequences disclose the same 687 amino acid-long sequence. Support for this assertion is found on pages 47-48 of the attached Sequence Report for Group 2, which compares the amino acid

sequence of SEQ ID NO:3 of the present application to SEQ ID NO:179 of the 7,314,971 patent and indicates a finding of 100% identity between the two sequences.

Furthermore, the nucleic acid sequence of SEQ ID NO:1 disclosed and claimed in the present application is a genomic DNA, a portion of which encodes a protein having the amino acid sequence of SEQ ID NO:3, see for example paragraphs [232] and [239] of the present application.

Accordingly, the claims of both the present application (claims 53, 105 and 106) and the 7,314,971 patent (claim 11) encompass the same nucleic acids. For this reason, it is believed an interference should be declared between the present application and the 7,314,971 patent.

Applicants Are The Senior Party Based On The Earliest Filed Priority Documents

The present application claims priority to: Japanese Application 2001-128008 (filed April 25, 2001); Japanese Application 2001-202082 (filed July 3, 2001); Japanese Application 2002-020083 (filed January 29, 2002); PCT Application PCT/JP02/04092 (filed April 24, 2002) and U.S. Application No.10/451,366 (filed April 24, 2002) which is a national stage of International Application No. PCT/JP02/04092. Certified copies of the Japanese priority applications have previously been submitted to the Patent Office. Copies of the foreign priority documents translated into English (with certificate of translation) are submitted herewith.

The 7,314,971 patent claims priority to: U.S. Provisional Application 60/305,026 (filed July 12, 2001); U.S. Provisional Application 60/305,363 (filed July 13, 2001); U.S. Provisional Application 60/308,736 (filed July 30, 2001); and U.S. Application 10/195,144 (filed July 12, 2002).

The 687 amino acid sequence of SEQ ID NO:3 of the present application was first disclosed by Applicants in its exact form as SEQ ID NO:3 in the sequence listing of Japanese Application 2002-020083 (filed January 29, 2002). It was also disclosed as SEQ ID NO:3 in the sequence listing of PCT Application PCT/JP02/04092 (filed on April

24, 2002) as well as SEQ ID NO:3 in the sequence listing of the U.S. Application No. 10/451,366 (filed April 24, 2002). An 804 amino acid sequence, having a 681 amino acid sequence having 100% sequence homology with a 681 sequence of SEQ ID NO:3 of the present application, was first disclosed by Applicants as SEQ ID NO:3 in the sequence listing of Japanese Application 2001-128008 (filed April 25, 2001). This 804 amino acid sequence was also disclosed as SEQ ID NO:3 in the sequence listing of Japanese Application 2001-202082 (filed July 3, 2001). Support for these assertions can be found on pages 49-52 of the attached Sequence Report for Group 3, which compares the amino acid sequence of SEQ ID NO:3 of the present application to SEQ ID NO:3 of each of the Japanese Applications (2001-128008; 2001-202082; and 2002-020083).

The 8553 nucleotide sequence of SEQ ID NO:1 of the present application was first disclosed by Applicants in its exact form as SEQ ID NO:1 in the sequence listing of Japanese Application 2001-128008 (filed April 25, 2001). It was also disclosed in its exact form as SEQ ID NO:1 in the sequence listing of Japanese Application 2001-202082 (filed July 3, 2001); as SEQ ID NO:1 in the sequence listing of Japanese Application 2002-020083 (filed January 29, 2002); as SEQ ID NO:1 in the sequence listing of PCT Application PCT/JP02/04092 (filed April 24, 2002) and U.S. Application No.10/451,366 (filed April 24, 2002). Support for these assertions can be found on pages 1-40 of the attached Sequence Report for Group 3, which compares the nucleic acid sequence of SEQ ID NO:1 of the present application to SEQ ID NO:1 of each of the Japanese Applications (2001-128008; 2001-202082; and 2002-020083).

Applicants disclosed the complete sequence of SEQ ID NO:3 on January 29, 2002 in the sequence listing of Japanese Application 2002-020083. This complete SEQ ID NO:3 was also disclosed in the sequence listing of PCT Application PCT/JP02/04092 filed on April 24, 2002, as well as in the sequence listing of the U.S. Application No. 10/451,366, filed April 24, 2002.

Brown et al. first disclosed the complete amino acid sequence of SEQ ID NO: 179 in the July 12, 2002 filing of U.S. Application 10/195,144. Thus, Applicants'

disclosures of SEQ ID NO:3 in its present form precedes the Brown et al. disclosure of SEQ ID NO:179.

In addition, Applicants disclosed the nucleic acid sequence of SEQ ID NO:1 in the sequence listing of Japanese Application 2001-128008 filed on April 25, 2001. As discussed above, SEQ ID NO:1 is a genomic DNA, a portion of which encodes a protein having the amino acid sequence of SEQ ID NO:3 (as stated on the final paragraph of page 37 of the as-filed specification). It is believed nucleotides 3754-8553 of SEQ ID NO:1 contain the coding sequence as well as a promoter and terminator necessary for gene expression, where nucleotides 3754-5091 are identifies as the promoter (pages 7-8 and 38 of the as-filed specification). SEQ ID NO:1 was also disclosed in each of the subsequent Japanese Patent applications and the PCT application. The earliest Brown et al. priority document was filed on July 12, 2001. Thus, Applicants' disclosure of a nucleic acid sequence encoding a protein comprising the sequence of SEQ ID NO:3 of the current application was prior to the earliest possible disclosure of a similar nucleic acid by Brown et al.

In the Office Communication of September 15, 2008, the Examiner stated that Provisional Application 60/305,026 (filed on July 13, 2001 by Brown et al.) contained amino acid sequence SEQ ID NO:4, which is a 686 amino acid-long protein, and a nucleic acid encoding it. The Examiner stated that because the protein set forth in SEQ ID NO:4 by Brown et al. appears to be at least 70% identical to Applicants' SEQ ID NO:3, and the encoding nucleic acid at least 70% identical to Applicants' SEQ ID NO:2, the Brown et al. applications may still be presumed to be the Senior Party on their face. Applicants respectfully submit this is erroneous. Moreover, as stated above, the present claims are limited to nucleotide sequences which are at least 90% homologous to nucleotide sequences which encode the amino acid of SEQ ID NO:1-3. It is respectfully submitted that even if, contrary to fact, Brown SEQ ID NO:4 were at least 70% identical to Applicants' SEQ ID NO:3, and the encoding nucleic acid at least 70% identical to Applicants' SEQ ID NO:2, this would be irrelevant to any issue of priority, in the absence of disclosure by Brown of a sequence that is at least 90% homologous to the nucleotide sequence defined by Applicant's claims (and an interference count).

As stated above, Brown et al. did not disclose the final complete amino acid sequence of SEQ ID NO:179 (which is the same as Applicants' SEQ ID NO:3) until July 12, 2002, several months after Applicants' disclosure of SEQ ID NO:3 in its final complete form. Additionally, the Japanese Applications filed by Applicants on April 24, 2001 (JP 2001-128008) and July 3, 2001 (JP 2001-202082) both disclose an 804 amino acid-long protein (labeled as SEQ ID NO:3 in both applications). This 804 amino acid sequence has a 681 amino acid sequence, amino acids positions 84-764, having 100% sequence homology with a 681 sequence, amino acid positions 1-681, of SEQ ID NO:3 of the present application. Support for this assertion can be found on pages 49-51 of the attached Sequence Report for Group 3, which compares SEQ ID NO:3 of the current application with SEQ ID NO:3 of Japanese Applications 2001-128008 and 2001-202082.

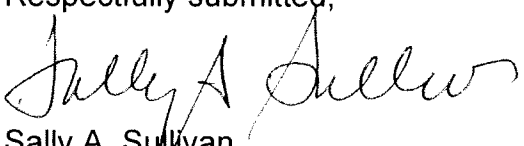
In contrast, the 686 amino acid protein disclosed in the Brown et al. Provisional Application 60/305,026 (filed July 13, 2001) has less than 90% sequence homology with SEQ ID NO:3 of the current application. Support for this assertion can be found on pages 116-117 of the attached Sequence Report for Group 5, which compares SEQ ID NO:3 of the present application with SEQ ID NO:4 of Provisional Application 60/305,026 and reports a sequence homology of 86%. Both of Japanese Applications 2001-128008 and 2001-202082 disclosing the homologous amino acid sequence to current SEQ ID NO:3 precede the July 13, 2001 filing by Brown et al.

In summary, Applicants' earliest disclosure of the complete amino acid sequence provided in SEQ ID NO:3 of the present application precedes the earliest such disclosure by Brown et al. Applicants' earliest disclosure of a nucleic acid (SEQ ID NO:1) encoding a protein comprising the sequence of SEQ ID NO:3 of the present invention precedes the earliest disclosure of any kind by Brown et al. Applicants' disclosure of an amino acid sequence having high homology to the amino acid sequence provided in SEQ ID NO:3 of the present application also precedes the earliest disclosure of any amino acid by Brown et al. Accordingly, Applicants should be considered the Senior Party.

Conclusion

It is believed that no fees are due for this submission. If, however, this is not correct, please charge any fees required, or credit any overpayment, to Deposit Account No. 07-1969.

Respectfully submitted,



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